

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 7, 2006, 16:07:40 ; Search time 0.001 Seconds  
(without alignments)  
2331.684 Million cell updates/sec

Title: US-10-665-715-16-COPY  
Perfect score: 2879  
Sequence: 1 MEPDSVIEDKTIELMCSVPR.....PPSAQNETRSPSRTYTYISR 542

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 1 seqs, 2151 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=soft -Q=eliz.pep -DB=y14153.gb\_pr -SUFFIX=pto  
-OUT=eliz.res -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext  
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO\_XLPXY -NEG\_SCORES=0  
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10  
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : y14153.gb\_pr:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	2384.5	82.8	2151	1	HSBTRCP	ACCESSION:Y14153
c	2	58	2.0	2151	1	HSBTRCP	ACCESSION:Y14153

ALIGNMENTS

## RESULT 1

## HSBTRCP

LOCUS HSBTRCP 2151 bp mRNA linear PRI 07-FEB-2003

DEFINITION Homo sapiens mRNA for beta-transducin repeat containing protein.

ACCESSION Y14153

VERSION Y14153.1 GI:2995193

KEYWORDS beta-transducin repeats; beta-TRCP gene; WD repeat.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE 1

AUTHORS Margottin,F., Bour,S.P., Durand,H., Selig,L., Benichou,S.,  
Richard,V., Thomas,D., Strebel,K. and Benarous,R.TITLE A novel human WD protein, h-beta TrCp, that interacts with HIV-1  
Vpu connects CD4 to the ER degradation pathway through an F-box  
motif

JOURNAL Mol. Cell 1 (4), 565-574 (1998)

PUBMED 9660940

## REFERENCE 2 (bases 1 to 2151)

AUTHORS Benarous,R.

TITLE Direct Submission

JOURNAL Submitted (03-JUL-1997) R. Benarous, INSERM - I.C.G.M., Laboratoire  
Interactions Proteiques, CHU Cochin, 24 rue de Fg.St-Jacques, 75014  
Paris, FRANCE

## FEATURES Location/Qualifiers

## source

1. .2151  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_line="Jurkat T-cell"  
/cell\_type="T lymphocyte"  
/tissue\_type="lymphoid"

## gene

1. .2151  
/gene="beta-TRCP"

## CDS

70. .1779  
/gene="beta-TRCP"  
/codon\_start=1  
/product="beta-transducin repeats containing protein"  
/protein\_id="CAA74572.1"  
/db\_xref="GI:2995194"  
/db\_xref="GOA:Q9Y297"  
/db\_xref="UniProtKB/Swiss-Prot:Q9Y297"  
/translation="MDPAEAVLQEKALKFMNSSEREDCNGEPPRKIIPEKNSLRQTY  
NSCARLCLNQETVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCV  
KYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLPMLQRDFITALPARGLDHIAENI  
LSYLDAKSLCAAELVCKEWYRVTS DGM LWKKLIERMVRTDSLWRGLAERRGWGQYLFK  
NKPPDGNAPPNSFYRALYPKIIQDIETIESNWRRCGRHSLQRIHCRSETSKGVYCLQYD  
DQKIVSGLRDNTIKIWDKNTLECKRI LTGHTGSVLCLQYDERV IITGSSDSTVRVWDV  
NTGEMLNTLIHCEAVLHLRFNNGMMVTC SKDRS IAVWDMASPTDITLRRVLVGHRAA  
VNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNHGKRGIAQLQYRDLVVGSSDN  
TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAG  
TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAQAEPSPSRPTYTY  
ISR"

## repeat\_region

259. .544

/rpt\_family="WD"  
/rpt\_unit\_range=516. .544

Alignment Scores:

Pred. No.:	0	Length:	2151
Score:	2384.50	Matches:	451
Percent Similarity:	87.4%	Conservative:	48
Best Local Similarity:	79.0%	Mismatches:	41
Query Match:	82.8%	Indels:	31
DB:	1	Gaps:	7

US-10-665-715-16-COPY (1-542) x HSBTRCP (1-2151)

```
Qy      1 MetGluPro---AspSerValIleGluAspLysThrIleGluLeuMetCysSer----- 17
      |||:::|||  :::::|||:::|||||  :::::  |||  |||
Db      70 ATGGACCCGCGCCGAGGCGGTGCTGCAAGAGAAGGCACTCAAGTTTATGAATTCCTCAGAG 129

Qy      18 -----ValPro----- 19
      ::|||
Db     130 AGAGAAGACTGTAATAATGGCGAACCCCTAGGAAGATAATACCAGAGAAGAATTCACCTT 189

Qy      20 ArgSerLeuTrpLeuGlyCysAlaAsnLeuVal-----GluSerMetCysAlaLeu 36
      |||  ::  |||||  |||  |||:::|||||
Db     190 AGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTTAGCA 249

Qy      37 SerCysLeuGlnSerMetProSerValArgCysLeu-----GlnIleSerAsnGly 53
      |||  ::|||  ::  |||::  :::|||||
Db     250 AGC-----ACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAACTTGCCAATGGC 303

Qy      54 ThrSerSerValIleValSerArgLysArgProSerGluGlyAsnTyrGlnLysGluLys 73
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     304 ACTTCCAGTATGATTGTGCCCAAGCAACGGAACTCTCAGCAAGCTATGAAAAGGAAAAG 363

Qy      74 AspLeuCysIleLysTyrPheAspGlnTrpSerGluSerAspGlnValGluPheValGlu 93
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     364 GAAGTGTGTGTCAAATACCTTTGAGCAGTGGTCAGAGTCAGATCAAGTGAATTTGTGGAA 423

Qy      94 HisLeuIleSerArgMetCysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysPro 113
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     424 CATCTTATATCCCAAATGTGTCTATTACCAACATGGGCACATAAACTCGTATCTTAAACCT 483

Qy     114 MetLeuGlnArgAspPheIleThrAlaLeuProGluGlnGlyLeuAspHisIleAlaGlu 133
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     484 ATGTTGCAGAGAGATTTCACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCTGAG 543

Qy     134 AsnIleLeuSerTyrLeuAspAlaArgSerLeuCysAlaAlaGluLeuValCysLysGlu 153
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     544 AACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAGGAA 603

Qy     154 TrpGlnArgValIleSerGluGlyMetLeuTrpLysLysLeuIleGluArgMetValArg 173
      |||  |||||  |||::|::|::|::|::|::|::|::|::|::|::|::|
Db     604 TGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTCAGG 663

Qy     174 ThrAspProLeuTrpLysGlyLeuSerGluArgArgGlyTrpAspGlnTyrLeuPheLys 193
      |||||  |||||::|::|::|::|::|::|::|::|::|::|::|::|
Db     664 ACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAGTATTTATTCAA 723
```

Qy	194	AsnArgProThrAspGly-----ProProAsnSerPheTyrArgSerLeuTyrProLys	211
		:::	
Db	724	AACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTATAGAGCACTTTATCCTAAA	783
Qy	212	IleIleGlnAspIleGluThrIleGluSerAsnTrpArgCysGlyArgHisAsnLeuGln	231
Db	784	ATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTTACAG	843
Qy	232	ArgIleGlnCysArgSerGluAsnSerLysGlyValTyrCysLeuGlnTyrAspAspGlu	251
Db	844	AGAATTCACCTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTCTTACAGTATGATGATCAG	903
Qy	252	LysIleIleSerGlyLeuArgAspAsnSerIleLysIleTrpAspLysThrSerLeuGlu	271
		::	
Db	904	AAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACATTGGAA	963
Qy	272	CysLeuLysValLeuThrGlyHisThrGlySerValLeuCysLeuGlnTyrAspGluArg	291
		:::::	
Db	964	TGCAAGCGAATTCTCACAGGCCATACAGGTTCACTCCTCTGTCTCCAGTATGATGAGAGA	1023
Qy	292	ValIleValThrGlySerSerAspSerThrValArgValTrpAspValAsnThrGlyGlu	311
		::	
Db	1024	GTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACAGGTGAA	1083
Qy	312	ValLeuAsnThrLeuIleHisHisAsnGluAlaValLeuHisLeuArgPheSerAsnGly	331
		:::	
Db	1084	ATGCTAAACACGTTGATTACCATTTGTGAAGCAGTTCTGCACCTTGCCTTTCATAATGGC	1143
Qy	332	LeuMetValThrCysSerLysAspArgSerIleAlaValTrpAspMetAlaSerAlaThr	351
		:::	
Db	1144	ATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCAACT	1203
Qy	352	AspIleThrLeuArgArgValLeuValGlyHisArgAlaAlaValAsnValValAspPhe	371
Db	1204	GACATTACCCTCCGGAGGGTGCTGGTTCGGACACCGAGCTGCTGTCAATGTTGTAGACTTT	1263
Qy	372	AspAspLysTyrIleValSerAlaSerGlyAspArgThrIleLysValTrpSerThrSer	391
Db	1264	GATGACAAGTACATTGTTTCTGCATCTGGGGATAGAATAAAAGGTATGGAACACAAGT	1323
Qy	392	ThrCysGluPheValArgThrLeuAsnGlyHisLysArgGlyIleAlaCysLeuGlnTyr	411
Db	1324	ACTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTAC	1383
Qy	412	ArgAspArgLeuValValSerGlySerSerAspAsnThrIleArgLeuTrpAspIleGlu	431
Db	1384	AGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAA	1443
Qy	432	CysGlyAlaCysLeuArgValLeuGluGlyHisGluGluLeuValArgCysIleArgPhe	451
Db	1444	TGTGGTGATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTTCGATTT	1503
Qy	452	AspAsnLysArgIleValSerGlyAlaTyrAspGlyLysIleLysValTrpAspLeuGln	471
Db	1504	GATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTTGTG	1563
Qy	472	AlaAlaLeuAspProArgAlaProAlaSerThrLeuCysLeuArgThrLeuValGluHis	491

```

      |||
Db      1564 GCTGCTTTGGACCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACCCCTTGTGGAGCAT 1623
      |||
Qy      492 SerGlyArgValPheArgLeuGlnPheAspGluPheGlnIleIleSerSerSerHisAsp 511
      |||
Db      1624 TCCGGAAGAGTTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGTAGTTCACATGAT 1683
      |||
Qy      512 AspThrIleLeuIleTrpAspPheLeuAsnValProProSerAlaGlnAsnGluThrArg 531
      |||
Db      1684 GACACAATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCAAGCTGAACCCCCCGT 1743
      |||
Qy      532 SerProSerArgThrTyrThrTyrIleSerArg 542
      |||
Db      1744 TCCCCTTCTCGAACATACACCTACATCTCCAGA 1776

```

## RESULT 2

### HSBTRCP/c

LOCUS HSBTRCP 2151 bp mRNA linear PRI 07-FEB-2003

DEFINITION Homo sapiens mRNA for beta-transducin repeat containing protein.

ACCESSION Y14153

VERSION Y14153.1 GI:2995193

KEYWORDS beta-transducin repeats; beta-TRCP gene; WD repeat.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

### REFERENCE 1

AUTHORS Margottin,F., Bour,S.P., Durand,H., Selig,L., Benichou,S.,  
Richard,V., Thomas,D., Strebel,K. and Benarous,R.

TITLE A novel human WD protein, h-beta TrCp, that interacts with HIV-1  
Vpu connects CD4 to the ER degradation pathway through an F-box  
motif

JOURNAL Mol. Cell 1 (4), 565-574 (1998)

PUBMED 9660940

### REFERENCE 2 (bases 1 to 2151)

AUTHORS Benarous,R.

TITLE Direct Submission

JOURNAL Submitted (03-JUL-1997) R. Benarous, INSERM - I.C.G.M., Laboratoire  
Interactions Proteiques, CHU Cochin, 24 rue de Fg.St-Jacques, 75014  
Paris, FRANCE

### FEATURES Location/Qualifiers

#### source

1. .2151  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_line="Jurkat T-cell"  
/cell\_type="T lymphocyte"  
/tissue\_type="lymphoid"

#### gene

1. .2151  
/gene="beta-TRCP"

#### CDS

70. .1779  
/gene="beta-TRCP"  
/codon\_start=1  
/product="beta-transducin repeats containing protein"  
/protein\_id="CAA74572.1"  
/db\_xref="GI:2995194"

```

/db_xref="GOA:Q9Y297"
/db_xref="UniProtKB/Swiss-Prot:Q9Y297"
/translation="MDPAEAVLQEKALKFMNSSEREDCNNGEPPrKI IPEKNSLRQTY
NSCARLCLNQETVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCV
KYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMQLQDFITALPARGLDHIAENI
LSYLDKSLCAAELVCKEYRVTS DGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFK
NKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYD
DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERV IITGSSDSTVRVWDV
NTGEMLNTLIHHCEAVLHLRFNNGMMVTC SKDRSIAVWDMASPTDITLRRVLVGHRAA
VNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNHGKRGIA CLQYRDLVVGSSDN
TIRLWDIECGACLRVLEGHEELVRCIRFDNKRI VSGAYDGKIKVWDLVAALDPRAPAG
TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAQAEPPRSPSRITYY
ISR"
repeat_region 259. .544
/rpt_family="WD"
/rpt_unit_range=516. .544

```

Alignment Scores:

Pred. No.:	0	Length:	2151
Score:	58.00	Matches:	83
Percent Similarity:	31.5%	Conservative:	52
Best Local Similarity:	19.4%	Mismatches:	137
Query Match:	2.0%	Indels:	158
DB:	1	Gaps:	21

US-10-665-715-16-COPY (1-542) x HSBTRCP (1-2151)

```

Qy      20 ArgSerLeuTrpLeuGlyCysAlaAsnLeuValGluSerMetCysAlaLeuSerCysLeu 39
      |||  |||  |||  |||  |||  ::  |||
Db      1970 AGACCGTCCTGGGCCGACTGCAGACCAACTGTGTCCCAACAGGAGTCTCAAAGC----- 1917

Qy      40 GlnSerMetProSerValArgCysLeuGlnIleSerAsnGlyThrSerSerValIleVal 59
      |||:::  |||  :::||  |||:::||  :::::
Db      1916 -----CCTGCTCCTCGGCTAGTCCAGGG-AAACTGGGCAGTAGTTTGATTGTTACT 1867

Qy      60 SerArgLysArgProSerGluGlyAsnTyrGlnLysGluLysAspLeu----- 75
      |||  |||  |||  |||  ::  |||
Db      1866 GTTGTTCCTCATCCTGGTATTGGCAGATACGTAAATACCGCAA-CTTTAATGGGTCCTG 1808

Qy      76 -----CysIleLysTyrPheAspGln 82
      |||  |||:::
Db      1807 GGCAAGTATGAGGTCAGTGTATGGTTATTTATCTGGAGATGTAGGTGTATGTTTCGAGAAG 1748

Qy      83 TrpSerGluSerAspGlnValGluPheValGluHisLeuIleSer-----ArgMet 99
      ::  |||:::  :::::|||||  |||  ::
Db      1747 GGGAACGGGGGGGTTTCAGCTTGGGCAGCTGGATCATTTAGGAAGTCCCAGATGAGGATTG 1688

Qy      100 CysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysProMetLeuGlnArgAspPhe 119
      |||||  |||:::||  |||  ::  ::  ::
Db      1687 TGTCAT-----CATGTGAAC---TACTGACAATCTGGAATTCATCAAAC TGTA 1643

Qy      120 IleThrAlaLeu-----ProGluGlnGlyLeuAspHisIleAlaGluAsnIle 135
      ::  |||  |||:::  ::||  :::::
Db      1642 GTCGAAAAACTCTTCCGGAATGCTCCACAAGGGTCCGTAGACAGAGTGTCC----- 1592

Qy      136 LeuSerTyrLeuAspAlaArgSerLeuCysAlaAlaGluLeuValCysLysGluTrpGln 155

```

Db 1592 ----- 1592  
 Qy 156 ArgValIleSerGluGlyMetLeuTrpLysLysLeuIleGluArgMetValArgThrAsp 175  
 Db 1592 ----- 1592  
 Qy 176 ProLeuTrpLysGlyLeuSerGluArgArgGlyTrpAspGlnTyr----- 190  
 Db 1591 -----CTGCAGGAGCACGGGGGTCCAAAGCAGCCACAAGATCCCACACTT 1547  
 Qy 191 ---LeuPheLysAsnArg-ProThrAspGlyProProAsnSerPheTyrArgSerLeuTy 209  
 Db 1546 TAATTTTTCATCATAGGCCCTGAC-----TA 1517  
 Qy 209 rProLysIleIleGlnAsp-IleGluThrIleGluSerAsnTrpArgCysGly----- 226  
 Db 1516 TCCTCTTGTTATCAAATCGAATACAACGCACCAATTCCTCATGGCCTTCTAACACTCGTA 1457  
 Qy 227 -----ArgHisAsnLeuGlnArgIleGlnCysArgSerGluAsnS 240  
 Db 1456 AACATGCACCACATTCTATGTCCATAATCTG----- 1425  
 Qy 240 erLysGlyValTyrCysLeuGlnTyrAspAspGluLysIleIleSerGlyLeuArgAspA 260  
 Db 1424 -----ATAGTGTGTGTCAGATGAGCCACTCACTACC----- 1395  
 Qy 260 snSerIleLysIleTrpAspLysThrSerLeuGluCysLeu-----LysValLeuT 277  
 Db 1394 --AGCCTGTCCCTGTACTGCAAACAGGCAATGCCTCGTTTGTGTCCATTTAAGGTCTCTTA 1337  
 Qy 277 hrGly-----HisThrGlySerValLeuCysLeuGlnTyrAspGluA 291  
 Db 1336 CAAATTCACAAGTACTTGTGTTCCATACC-----TTTATAGTTCTATCCCCAGATGCAG 1283  
 Qy 291 rgValIleValThrGlySerSerAspSerThrValArgValTrpAspValAsnThrGlyG 311  
 Db 1282 AAACAATGTACTTGTCTATCAAAGTCTACAACATTGACAGCAGCTCGGTGTCCGACC---A 1226  
 Qy 311 luValLeuAsnThrLeuIleHisHisAsnGluAlaValLeuHisLeuArgPheSerAsnG 331  
 Db 1225 GCACCCTCCGAGGGTAATGTCTAGTTGGGGAGGCCATATCCCATACAGCAATGGAACGAT 1166  
 Qy 331 lyLeu---MetValThrCys-----SerLysAspArgSerIleAlaValT 345  
 Db 1165 CTTTGGAGCAGGTCACCATCATGCCATTATTGAAACGCAAGTGCAGAACTGCTTCACAAT 1106  
 Qy 345 rpAspMetAlaSerAlaThrAspIleThrLeuArgArgValLeuValGlyHisArgAlaA 365  
 Db 1105 GGTGAATC-----AACGTGTTTAGCATTTACCTGTATTTACATCCCACACTCTG- 1056  
 Qy 365 laValAsnValValAspPheAspAspLysTyrIleValSerAlaSerGly-----A 382  
 Db 1055 -----ACCGTGGAATCCGATGATCCTGTTATGATCACTCTCTCATCACTGGAGAC 1004  
 Qy 382 spArgThrIleLysValTrp 388  
 Db 1003 AGAGGACTGAACCTGTATGG 984

Search completed: September 7, 2006, 16:07:41  
Job time : 1 secs